

CERTIFICATE OF MAILING

I hereby certify that this paper (along with any paper referred to as being attached or enclosed) is being deposited with the United States Postal Service on the date shown below with sufficient postage as first class mail in an envelope addressed to the Assistant Commissioner for Patents, Washington, D.C. 20231.

Stephen C. D'Amico
Type or print name

Signature

January 30, 2002
Date

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

IN RE APPLICATION OF

FEDER ET AL.

APPLICATION NO: 09/966,459

FILED: SEPTEMBER 26, 2001

FOR: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY4,
EXPRESSED HIGHLY IN PROSTATE, COLON, AND LUNGAssistant Commissioner for Patents
Washington, D.C. 20231SUBMISSION OF SUBSTITUTE SEQUENCE LISTING INCLUDING STATEMENT OF
VERIFICATION IN RESPONSE TO MISSING PARTS NOTICE

Sir:

In response to the Notice to File Missing Parts of Application, the Sequence Listing has been amended to make it compliant with C.F.R. 1.822 and 1.823. Support for the amendments can be found in the specification, as originally filed, and the Sequence Listing, as originally submitted. Respectfully, no new matter has been added.

Applicants request the originally submitted paper copy and Computer Readable Form of the Sequence Listing be replaced with the paper copy and Computer Readable Form of the Substitute Sequence Listing submitted herewith. Applicants believe the Substitute Sequence Listing is in compliance with C.F.R. 1.822 and 1.823.

Applicants hereby provide a Computer Readable Form of the Substitute Sequence Listing as well as the Paper Copy thereof. The undersigned states that the Substitute Paper Copy and the Substitute Computer Readable Form, submitted in accordance with 37 CFR §1.821(c) and (e), respectively, are the same.

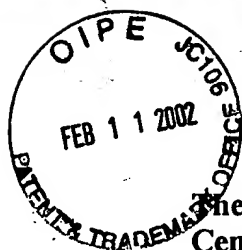
Respectfully submitted,

Bristol-Myers Squibb Company
Patent Department
P.O. Box 4000
Princeton, NJ 08543-4000
(609) 252-5289
Date: January 30, 2002

Stephen C. D'Amico
Agent for Applicants
Reg. No. 46,652



RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/966,459
Source: OIP/E
Date Processed by STIC: 11/7/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/966,459

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SO:

- 1 Wrapped Nucleics
 Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering
The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length
Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's
 (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220>
Sequence(s) 30 missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.



OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/966,459

DATE: 11/07/2001

TIME: 14:24:55

Input Set : A:\30534111.app

Output Set: N:\CRF3\11072001\I966459.raw

Does Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: FEDER, J.N.
 4 MINTIER, G.
 5 RAMANATHAN, C.S.
 6 HAWKEN, D.R.
 7 CACACE, A.
 8 BARBER, L.
 9 KORNACKER, M.G.
 11 <120> TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY4,
 12 EXPRESSED HIGHLY IN PROSTATE, COLON, AND LUNG
 14 <130> FILE REFERENCE: D0039NP/3053-4117US3
 16 <140> CURRENT APPLICATION NUMBER: US/09/966,459
 17 <141> CURRENT FILING DATE: 2001-09-26
 19 <150> PRIOR APPLICATION NUMBER: 60/235,833
 20 <151> PRIOR FILING DATE: 2000-09-27
 22 <150> PRIOR APPLICATION NUMBER: 60/261,776
 23 <151> PRIOR FILING DATE: 2001-01-16
 25 <150> PRIOR APPLICATION NUMBER: 60/305,351
 26 <151> PRIOR FILING DATE: 2001-07-13
 28 <150> PRIOR APPLICATION NUMBER: 60/313,202
 29 <151> PRIOR FILING DATE: 2001-08-17
 31 <160> NUMBER OF SEQ ID NOS: 60
 33 <170> SOFTWARE: PatentIn Ver. 2.1

ERRORED SEQUENCES

718 <210> SEQ ID NO: 15
 719 <211> LENGTH: 318
 720 <212> TYPE: PRT
 721 <213> ORGANISM: MOUSE
 723 <400> SEQUENCE: 15
 724 Met Ser Pro Gly Asn Ser Ser Trp Ile His Pro Ser Ser Phe Leu Leu
 725 1 5 10 15
 727 Leu Gly Ile Pro Gly Leu Glu Glu Leu Gln Phe Trp Leu Gly Leu Pro
 728 20 25 30
 730 Phe Gly Thr Val Tyr Leu Ile Ala Val Leu Gly Asn Val Ile Ile Leu
 731 35 40 45
 733 Phe Val Ile Tyr Leu Glu His Ser Leu His Gln Pro Met Phe Tyr Leu
 734 50 55 60
 736 Leu Ala Ile Leu Ala Val Thr Asp Leu Gly Leu Ser Thr Ala Thr Val
 737 65 70 75 80
 739 Pro Arg Ala Leu Gly Ile Phe Trp Phe Gly Phe His Lys Ile Ala Phe
 740 85 90 95
 742 Arg Asp Cys Val Ala Gln Met Phe Phe Ile His Leu Phe Thr Gly Ile
 743 100 105 110
 745 Glu Thr Phe Met Leu Val Ala Met Ala Phe Asp Arg Tyr Ile Ala Ile
 746 115 120 125

RAW SEQUENCE LISTING

DATE: 11/07/2001

PATENT APPLICATION: US/09/966,459

TIME: 14:24:55

Input Set : A:\30534111.app

Output Set: N:\CRF3\11072001\I966459.raw

```

748 Cys Asn Pro Leu Arg Tyr Asn Thr Ile Leu Thr Asn Arg Thr Ile Cys
749      130      135      140
751 Ile Ile Val Gly Val Gly Leu Phe Lys Asn Phe Ile Leu Val Phe Pro
752 145      150      155      160
754 Leu Ile Phe Leu Ile Leu Arg Leu Ser Phe Cys Gly His Asn Ile Ile
755      165      170      175
757 Pro His Thr Tyr Cys Glu His Met Gly Ile Ala Arg Leu Ala Cys Val
758      180      185      190
760 Ser Ile Lys Val Asn Val Leu Phe Gly Leu Ile Leu Ile Ser Met Ile
761      195      200      205
763 Leu Leu Asp Val Val Leu Ser Ala Leu Ser Tyr Ala Lys Ile Leu His
764      210      215      220
766 Ala Val Phe Lys Leu Pro Ser Trp Glu Ala Arg Leu Lys Ala Leu Asn
767 225      230      235      240
769 Thr Cys Gly Ser His Val Cys Val Ile Leu Ala Phe Phe Thr Pro Ala
770      245      250      255
772 Phe Phe Ser Phe Leu Thr His Arg Phe Gly His Asn Ile Pro Arg Tyr
773      260      265      270
E--> 775 Ile His Ile Leu Leu Ala Asn Leu Tyr Val Ile Ile Pro Xaa Ala Leu
776      275      280      285
778 Asn Pro Ile Ile Tyr Gly Val Arg Thr Lys Gln Ile Gln Asp Arg Ala
779      290      295      300
781 Val Thr Ile Leu Cys Asn Glu Val Gly Gln Leu Ala Asp Asp
782 305      310      315

```

*see item 9 on Error
Summary
Sheet*

see next page for more errors

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<210> 30

<211> 39

<212> DNA

<213> Artificial Sequence

see item 11 on Euro summary sheet

<400> 30

cccaagcttg caccatgatg gtggatccca atggcattg

39

FYI →

Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence using n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/966,459

DATE: 11/07/2001

TIME: 14:24:56

Input Set : A:\30534111.app

Output Set: N:\CRF3\11072001\I966459.raw

L:16 M:270 C: Current Application Number differs, Replaced Current Application Number
L:775 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:15
L:1043 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:1043 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:1268 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:46
L:1268 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:46
L:1268 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46
L:1269 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:46
L:1269 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:46
L:1269 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46
L:1282 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:47
L:1282 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:47
L:1282 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:47
L:1283 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:47
L:1283 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:47
L:1283 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:47